



SEQUENCE LISTING

Lorens, James B.
Atchison, Robert E.
Frieria, Anabella
Holland, Sacha
Rigel Pharmaceuticals, Inc.

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<141> 2003-10-29

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 transforming sequence/gene; oncogene AXL

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 35 40 45
 Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
 50 55 60
 Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
 65 70 75 80
 Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
 85 90 95
 Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
 100 105 110
 Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
 115 120 125
 Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
 130 135 140
 Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
 145 150 155 160
 Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
 165 170 175
 Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
 180 185 190
 His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His
 195 200 205
 Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
 210 215 220
 Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
 225 230 235 240
 Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr
 245 250 255
 His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln
 260 265 270

Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser
 275 280 285
 Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Thr Pro
 290 295 300
 Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp
 305 310 315 320
 Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro
 325 330 335
 Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His
 340 345 350
 Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg
 355 360 365
 Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly
 370 375 380
 Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser
 385 390 395 400
 Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
 405 410 415
 Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Val Lys Glu Pro
 420 425 430
 Ser Thr Pro Ala Phe Ser Trp Pro Trp Trp Tyr Val Leu Leu Gly Ala
 435 440 445
 Val Val Ala Ala Ala Cys Val Leu Ile Leu Ala Leu Phe Leu Val His
 450 455 460
 Arg Arg Lys Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu Pro Thr Val
 465 470 475 480
 Glu Arg Gly Glu Leu Val Val Arg Tyr Arg Val Arg Lys Ser Tyr Ser
 485 490 495
 Arg Arg Thr Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile Ser Glu Glu
 500 505 510
 Leu Lys Glu Lys Leu Arg Asp Val Met Val Asp Arg His Lys Val Ala
 515 520 525
 Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly Ala Val Met Glu Gly
 530 535 540
 Gln Leu Asn Gln Asp Asp Ser Ile Leu Lys Val Ala Val Lys Thr Met
 545 550 555 560
 Lys Ile Ala Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe Leu Ser Glu
 565 570 575
 Ala Val Cys Met Lys Glu Phe Asp His Pro Asn Val Met Arg Leu Ile
 580 585 590

Gly Val Cys Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro Ala Pro Val
 595 600 605
 Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ser Phe Leu Leu
 610 615 620
 Tyr Ser Arg Leu Gly Asp Gln Pro Val Tyr Leu Pro Thr Gln Met Leu
 625 630 635 640
 Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr Leu Ser Thr
 645 650 655
 Lys Arg Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asn
 660 665 670
 Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile
 675 680 685
 Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val
 690 695 700
 Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys
 705 710 715 720
 Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg
 725 730 735
 Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr
 740 745 750
 Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly
 755 760 765
 Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg
 770 775 780
 Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala
 785 790 795 800
 Leu Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp
 805 810 815
 Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala Asp
 820 825 830
 Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr Ala
 835 840 845
 Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr Thr
 850 855 860
 Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro Gly
 865 870 875 880
 Gln Glu Asp Gly Ala
 885

<210> 7
 <211> 266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic tubulin
 cofactor D GH1-13-PCR-G3F1

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 ctgcagcgtc ccatccatgg tgatgacccc ctgcatggtc tggaaggagg aacggggccag 180
 attgcacagg ctccagtcca ggaactcagc catcttgctt tgcttgacat caggacgtgt 240
 gataaatctg gacacaagga cagcag 266

<210> 8
 <211> 3927
 <212> DNA
 <213> Homo sapiens

<220>
 <223> tubulin-specific chaperone d (TBCD), tubulin
 cofactor D cDNA

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 cgacgaaccg gccgcgggtg gccccgagga ggaggcggag gacgagacac tggcctttgg 180
 cgcgccgctg gaagcggttcg gcgagagcgc ggagaccggg gcgctgctgg gccgcctgag 240
 ggaggtgcac ggcggcgggcg cggagcgcgga ggtggccctg gagcggttcc gcgtaataat 300
 ggacaaatac caggagcagc ctcatctggt ggacccgcac cttgaatgga tgatgaactt 360
 gttgtttggac atagtgcagg atcagacatc tccagcttcc cttgtacatc tggcttttaa 420
 atttctttac atcatcacca aggttcgagg ctataaaaaca tttcttcgtt tatttcttca 480
 tgaagttgcc gatgtagagc ctgttttaga tttggtcaca attcagaatc ccaaggacca 540
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 cataatggac cgtattctcc aaatagcaga gtccactctg attgtcagtg acaaggcccc 720
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 gaccgaagat gacgacgaag atgacgacgt cccagagggg gtggagcgtg tgatagagca 1200
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 gaggtgctg tccatgacac tgagtccaga tcttcacatg aggcattggg cgattctcgc 1980
 ctgcgcagaa gttgcttacg ccttgtacaa acttgcagcc caagagaaca ggcccgtcac 2040

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gtgcttecta taaaatcatg taccaag 3927

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<210> 9
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> beta-tubulin cofactor D

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      35                      40                      45

Gly Gly Ala Glu Arg Glu Val Ala Leu Glu Arg Phe Arg Val Ile Met
      50                      55                      60

Asp Lys Tyr Gln Glu Gln Pro His Leu Leu Asp Pro His Leu Glu Trp
      65                      70                      75                      80

Met Met Asn Leu Leu Leu Asp Ile Val Gln Asp Gln Thr Ser Pro Ala
      85                      90                      95

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Ser Leu Val His Leu Ala Phe Lys Phe Leu Tyr Ile Ile Thr Lys Val
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 Arg Gly Tyr Lys Thr Phe Leu Arg Leu Phe Pro His Glu Val Ala Asp
 115 120 125
 Val Glu Pro Val Leu Asp Leu Val Thr Ile Gln Asn Pro Lys Asp His
 130 135 140
 Glu Ala Trp Glu Thr Arg Tyr Met Leu Leu Leu Trp Leu Ser Val Thr
 145 150 155 160
 Cys Leu Ile Pro Phe Asp Phe Ser Arg Leu Asp Gly Asn Leu Leu Thr
 165 170 175
 Gln Pro Gly Gln Ala Arg Met Ser Ile Met Asp Arg Ile Leu Gln Ile
 180 185 190
 Ala Glu Ser Tyr Leu Ile Val Ser Asp Lys Ala Arg Asp Ala Ala Ala
 195 200 205
 Val Leu Val Ser Arg Phe Ile Thr Arg Pro Asp Val Lys Gln Ser Lys
 210 215 220
 Met Ala Glu Phe Leu Asp Trp Ser Leu Cys Asn Leu Ala Arg Ser Ser
 225 230 235 240
 Phe Gln Thr Met Gln Gly Val Ile Thr Met Asp Gly Thr Leu Gln Ala
 245 250 255
 Leu Ala Gln Ile Phe Lys His Gly Lys Arg Glu Asp Cys Leu Pro Tyr
 260 265 270
 Ala Ala Thr Val Leu Arg Cys Leu Asp Gly Cys Arg Leu Pro Glu Ser
 275 280 285
 Asn Gln Thr Leu Leu Arg Lys Leu Gly Val Lys Leu Val Gln Arg Leu
 290 295 300
 Gly Leu Thr Phe Leu Lys Pro Lys Val Ala Ala Trp Arg Tyr Gln Arg
 305 310 315 320
 Gly Cys Arg Ser Leu Ala Ala Asn Leu Gln Leu Leu Thr Gln Gly Gln
 325 330 335
 Ser Glu Gln Lys Pro Leu Ile Leu Thr Glu Asp Asp Asp Glu Asp Asp
 340 345 350
 Asp Val Pro Glu Gly Val Glu Arg Val Ile Glu Gln Leu Leu Val Gly
 355 360 365
 Leu Lys Asp Lys Asp Thr Val Val Arg Trp Ser Ala Ala Lys Gly Ile
 370 375 380
 Gly Arg Met Ala Gly Arg Leu Pro Arg Ala Leu Ala Asp Asp Val Val
 385 390 395 400
 Gly Ser Val Leu Asp Cys Phe Ser Phe Gln Glu Thr Asp Lys Ala Trp
 405 410 415

His Gly Gly Cys Leu Ala Leu Ala Glu Leu Gly Arg Arg Gly Leu Leu
 420 425 430
 Leu Pro Ser Arg Leu Val Asp Val Val Ala Val Ile Leu Lys Ala Leu
 435 440 445
 Thr Tyr Asp Glu Lys Arg Gly Ala Cys Ser Val Gly Thr Asn Val Arg
 450 455 460
 Asp Ala Ala Cys Tyr Val Cys Cys Ala Phe Ala Arg Ala Tyr Glu Pro
 465 470 475 480
 Gln Glu Leu Lys Pro Phe Val Thr Ala Ile Ser Ser Ala Leu Val Ile
 485 490 495
 Ala Ala Val Phe Asp Arg Asp Ile Asn Cys Arg Arg Ala Ala Ser Ala
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 Ala Phe Gln Glu Asn Val Gly Arg Gln Gly Thr Phe Pro His Gly Ile
 515 520 525
 Asp Ile Leu Thr Thr Ala Asp Tyr Phe Ala Val Gly Asn Arg Ser Asn
 530 535 540
 Cys Phe Leu Val Ile Ser Val Phe Ile Ala Gly Phe Pro Glu Tyr Thr
 545 550 555 560
 Gln Pro Met Ile Asp His Leu Val Thr Met Lys Ile Ser His Trp Asp
 565 570 575
 Gly Val Ile Arg Glu Leu Ala Ala Arg Ala Leu His Asn Leu Ala Gln
 580 585 590
 Gln Ala Pro Glu Phe Ser Ala Thr Gln Val Phe Pro Arg Leu Leu Ser
 595 600 605
 Met Thr Leu Ser Pro Asp Leu His Met Arg His Gly Ser Ile Leu Ala
 610 615 620
 Cys Ala Glu Val Ala Tyr Ala Leu Tyr Lys Leu Ala Ala Gln Glu Asn
 625 630 635 640
 Arg Pro Val Thr Asp His Leu Asp Glu Gln Ala Val Gln Gly Leu Lys
 645 650 655
 Gln Ile His Gln Gln Leu Tyr Asp Arg Gln Leu Tyr Arg Gly Leu Gly
 660 665 670
 Gly Gln Leu Met Arg Gln Ala Val Cys Val Leu Ile Glu Lys Leu Ser
 675 680 685
 Leu Ser Lys Met Pro Phe Arg Gly Asp Thr Val Ile Asp Gly Trp Gln
 690 695 700
 Trp Leu Ile Asn Asp Thr Leu Arg His Leu His Leu Ile Ser Ser His
 705 710 715 720
 Ser Arg Gln Gln Met Lys Asp Ala Ala Val Ser Ala Leu Ala Ala Leu
 725 730 735

Cys Ser Glu Tyr Tyr Met Lys Glu Pro Gly Glu Ala Asp Pro Ala Ile
 740 745 750
 Gln Glu Glu Leu Ile Thr Gln Tyr Leu Ala Glu Leu Arg Asn Pro Glu
 755 760 765
 Glu Met Thr Arg Cys Gly Phe Ser Leu Ala Leu Gly Ala Leu Pro Gly
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 Phe Leu Leu Lys Gly Arg Leu Gln Gln Val Leu Thr Gly Leu Arg Ala
 785 790 795 800
 Val Thr His Thr Ser Pro Glu Asp Val Ser Phe Ala Glu Ser Arg Arg
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 Ala Gly Ala Pro Asp Glu Ala Val Cys Gly Glu Asn Val Ser Gln Ile
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 Tyr Cys Ala Leu Leu Gly Cys Met Asp Asp Tyr Thr Thr Asp Ser Arg
 850 855 860
 Gly Asp Val Gly Thr Trp Val Arg Lys Ala Ala Met Thr Ser Leu Met
 865 870 875 880
 Asp Leu Thr Leu Leu Leu Ala Arg Ser Gln Pro Glu Leu Ile Glu Ala
 885 890 895
 His Thr Cys Glu Arg Ile Met Cys Cys Val Ala Gln Gln Ala Ser Glu
 900 905 910
 Lys Ile Asp Arg Phe Arg Ala His Ala Ala Ser Val Phe Leu Thr Leu
 915 920 925
 Leu His Phe Asp Ser Pro Pro Ile Pro His Val Pro His Arg Gly Glu
 930 935 940
 Leu Glu Lys Leu Phe Pro Arg Ser Asp Val Ala Ser Val Asn Trp Ser
 945 950 955 960
 Ala Pro Ser Gln Ala Phe Pro Arg Ile Thr Gln Leu Leu Gly Leu Pro
 965 970 975
 Thr Tyr Arg Tyr His Val Leu Leu Gly Leu Val Val Ser Leu Gly Gly
 980 985 990
 Leu Thr Glu Ser Thr Ile Arg His Ser Thr Gln Ser Leu Phe Glu Tyr
 995 1000 1005
 Met Lys Gly Ile Gln Ser Asp Pro Gln Ala Leu Gly Ser Phe Ser Gly
 1010 1015 1020
 Thr Leu Leu Gln Ile Phe Glu Asp Asn Leu Leu Asn Glu Arg Val Ser
 1025 1030 1035 1040
 Val Pro Leu Leu Lys Thr Leu Asp His Val Leu Thr His Gly Cys Phe
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Asp Ile Phe Thr Thr Glu Glu Asp His Pro Phe Ala Val Lys Leu Leu
 1060 1065 1070

Ala Leu Cys Lys Lys Glu Ile Lys Asn Ser Lys Asp Ile Gln Lys Leu
 1075 1080 1085

Leu Ser Gly Ile Ala Val Phe Cys Gly Met Val Gln Phe Pro Gly Asp
 1090 1095 1100

Val Arg Arg Gln Ala Leu Leu Gln Leu Cys Leu Leu Leu Cys His Arg
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Phe Pro Leu Ile Arg Lys Thr Thr Ala Ser Gln Val Tyr Glu Thr Leu
 1125 1130 1135

Leu Thr Tyr Ser Asp Val Val Gly Ala Asp Val Leu Asp Glu Val Val
 1140 1145 1150

Thr Val Leu Ser Asp Thr Ala Trp Asp Ala Glu Leu Ala Val Val Arg
 1155 1160 1165

Glu Gln Arg Asn Arg Leu Cys Asp Leu Leu Gly Val Pro Arg Pro Gln
 1170 1175 1180

Leu Val Pro Gln Pro Gly Ala Cys
 1185 1190

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
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 atgcccaggc acctcagcac tgtgcaggcc acggcggcaa gaccagcac tggccatact 180
 tgacgcgctg gcagccgtgg ttcttccagc gccgcaggat gtccacgctg ccgatccagg 240
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<210> 11
 <211> 687
 <212> PRT
 <213> Homo sapiens

<220>
 <223> transglutaminase 2, protein-glutamine
 gamma-glutamyltransferase, tissue transglutaminase
 (TGase C, TGC, TGase-H)

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 35 40 45
 Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
 50 55 60
 Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
 65 70 75 80
 Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
 85 90 95
 Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
 100 105 110
 Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
 115 120 125
 Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
 130 135 140
 Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
 145 150 155 160
 Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
 165 170 175
 Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
 180 185 190
 Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
 195 200 205
 Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
 210 215 220
 Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
 225 230 235 240
 Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
 245 250 255
 Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
 260 265 270
 Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
 275 280 285
 Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
 290 295 300
 His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
 305 310 315 320
 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
 325 330 335

Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
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 Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
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 Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
 370 375 380
 Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
 385 390 395 400
 Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
 405 410 415
 Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
 420 425 430
 Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
 435 440 445
 Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
 450 455 460
 Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
 465 470 475 480
 Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
 485 490 495
 Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg
 500 505 510
 Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
 515 520 525
 Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu
 530 535 540
 Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
 545 550 555 560
 Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
 565 570 575
 Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
 580 585 590
 Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
 595 600 605
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 645 650 655

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675 680 685

<210> 12
<211> 3257
<212> DNA
<213> Homo sapiens

<220>
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protein-glutamine gamma-glutamyltransferase (TGM2)
cDNA

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<212> PRT

<213> Homo sapiens

<220>

<223> transglutaminase 2, C polypeptide,
protein-glutamine-gamma-glutamyltransferase

<400> 13

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Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
  35              40              45

Asn Tyr Gln Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
  50              55              60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
  65              70              75              80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
  85              90              95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
 100              105              110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
 115              120              125

Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
 130              135              140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
 145              150              155              160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
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Asn Ile Pro Trp Asn Phe Gly Gln Phe Gln Asp Gly Ile Leu Asp Ile
 180              185              190

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 225 230 235 240
 Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
 245 250 255
 Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
 260 265 270
 Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
 275 280 285
 Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
 290 295 300
 His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
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 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
 325 330 335
 Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
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 Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
 355 360 365
 Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
 370 375 380
 Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
 385 390 395 400
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 405 410 415
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 Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
 435 440 445
 Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
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 465 470 475 480
 Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
 485 490 495
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 500 505 510

Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
 515 520 525
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 530 535 540
 Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
 545 550 555 560
 Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
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 Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
 580 585 590
 Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
 595 600 605
 Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
 610 615 620
 Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
 625 630 635 640
 Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Val Pro
 645 650 655
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<210> 14
 <211> 1781
 <212> DNA
 <213> Homo sapiens

<220>
 <223> similar to transglutaminase 2, C polypeptide,
 protein-glutamine-gamma-glutamyltransferase, clone
 MGC:1193 cDNA

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<210> 15

<211> 548

<212> PRT

<213> Homo sapiens

<220>

<223> similar to transglutaminase 2, C polypeptide,
protein-glutamine gamma-glutamyltransferase

<400> 15

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Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr
  1              5              10              15

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Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val
      20              25              30

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Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
      35              40              45

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Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
      50              55              60

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Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
      65              70              75              80

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Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
      85              90              95

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Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
      100              105              110

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Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
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Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
      130              135              140

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Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
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Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
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Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
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 225 230 235 240
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 245 250 255
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 260 265 270
 Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
 275 280 285
 Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
 290 295 300
 His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
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 Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
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 355 360 365
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 Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
 385 390 395 400
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 Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
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Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
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Trp Ser Ile Cys
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 <223> transglutaminase

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 Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
 50 55 60
 Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
 65 70 75 80
 Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
 85 90 95
 Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
 100 105 110
 Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
 115 120 125
 Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
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 Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
 145 150 155 160
 Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
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 Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
 180 185 190
 Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
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 Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Trp
 210 215 220
 Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
 225 230 235 240
 Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
 245 250 255
 Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
 260 265 270
 Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
 275 280 285
 Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
 290 295 300
 His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
 305 310 315 320

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Tyr	Cys	Cys	Gly	Pro	Val	Pro	Val	Arg	Ala	Ile	Lys	Glu	Gly	Asp	Leu	
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Ser	Thr	Lys	Tyr	Asp	Ala	Pro	Phe	Val	Phe	Ala	Glu	Val	Asn	Ala	Asp	
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Arg	Asp	Glu	Arg	Glu	Asp	Ile	Thr	His	Thr	Tyr	Lys	Tyr	Pro	Glu	Gly	
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<212> DNA
<213> Artificial Sequence
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<220>
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deaminase GH1-27-PCR-G3F1

<400> 18						
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taaatacc	gatagtga	aggcaact	tgcgaggt	ctgttta	tggcgggg	240
gacattcc	aaattcat	cgaagtgc	caagattg	attgact	attcaatta	300

```

cagcagaccg agtcaaaaagc ttcagtgagt tacatctcat tcaatctcca gaagattggg 360
attatcgtct tctaagaggt tgctaatagcc tttcatcttg aagttacaca taacttctta 420
ctagccagta tggcaaaaagt aggcattctta agaataataa gcctccaatc ttccttactg 480
tctctcttgt cacatggaat ctacatgtgt ttgaactatt gctttaggga tttaaaatag 540
gggagcctgt ggtggcctgg tgcacagggg ctagaacgag agtgcctccc cttcttgtgt 600
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cgatccggca g 671

```

<210> 19

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<223> deoxycytidylate deaminase, dCMP deaminase (DCTD)

<400> 19

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Met Ser Glu Val Ser Cys Lys Lys Arg Asp Asp Tyr Leu Glu Trp Pro
  1              5              10              15

```

```

Glu Tyr Phe Met Ala Val Ala Phe Leu Ser Ala Gln Arg Ser Lys Asp
          20              25              30

```

```

Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
      35              40              45

```

```

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
      50              55              60

```

```

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
      65              70              75              80

```

```

Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
          85              90              95

```

```

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
          100              105              110

```

```

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Met
      115              120              125

```

```

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
      130              135              140

```

```

Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
      145              150              155              160

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```

Lys Ile Val Ile Asp Phe Asp Ser Ile Asn Ser Arg Pro Ser Gln Lys
          165              170              175

```

Leu Gln

<210> 20

<211> 1831

<212> DNA

<213> Homo sapiens

<220>

<223> dCMP deaminase (DCTD) cDNA

<400> 20

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atcgtgaatt cagaaaaaaa gattgtcggg attgggtaca atgggatgcc aaatgggtgc 180
agtgatgacg tggtgccttg gagaaggaca gcagagaata agctggacac caaatacccg 240
tacgtgtgcc atgcggagct gaatgccatc atgaacaaaa attcgaccga tgtgaaaggc 300
tgtagtatgt atgtcgcctt gttcccttgt aatgaatgcg ctaagctcat catccaggca 360
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```

<210> 21

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<223> dCMP deaminase (DCTD)

<400> 21

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Met Ser Glu Val Ser Cys Lys Lys Arg Asp Asp Tyr Leu Glu Trp Pro
  1              5              10              15

Glu Tyr Phe Met Ala Val Ala Phe Leu Ser Ala Gln Arg Ser Lys Asp
      20              25              30

Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
      35              40              45

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
      50              55              60

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
      65              70              75              80

Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
      85              90              95

```

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
 100 105 110

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Thr
 115 120 125

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
 130 135 140

Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
 145 150 155 160

Lys Ile Val Ile Asp Phe Asp Ser Ile Asn Ser Arg Pro Ser Gln Lys
 165 170 175

Leu Gln

<210> 22
 <211> 688
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic peptidase
 M41 (paraplegin) GH1-40-PCR-G3F1

<220>
 <221> modified_base
 <222> (1)..(688)
 <223> n = g, a, c or t

<400> 22
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 gttttccgctc tggccgggat gactggaagg gaagggtggat tcagtgcctt taatcagctt 120
 aaaatggctc gtttcacat tgtggattgg aagatgggga aaggagagtc gcttcaaaga 180
 cgtggcagga atgcacgaag ccaaactgga agtcgcgag tttgtggatt atctgaagag 240
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 ctgggaccgg gacgtcttct ttgatctc 688

<210> 23
 <211> 3087
 <212> DNA
 <213> Homo sapiens

<220>
 <223> spastic paraplegia 7, paraplegin (pure and
 complicated autosomal recessive) (SPG7) cDNA

<400> 23
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 cccgggaggg ggccggcgta catggccagc aggcctccg gggacctcg cgaggctgga 180
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aagggcgagg tgcagcgctg ccaggtggtg cctgagagcg acgtggtgga agtctacctg 600
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<210> 24

<211> 795

<212> PRT

<213> Homo sapiens

<220>

<223> paraplegin

<400> 24

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1

5

10

15

Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
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 Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
 35 40 45
 Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
 50 55 60
 Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
 65 70 75 80
 Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
 85 90 95
 Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
 100 105 110
 Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Glu Glu Arg
 115 120 125
 Arg Arg Arg Glu Arg Asp Asp Gln Met Tyr Arg Glu Arg Leu Arg Thr
 130 135 140
 Leu Leu Val Ile Ala Val Val Met Ser Leu Leu Asn Ala Leu Ser Thr
 145 150 155 160
 Ser Gly Gly Ser Ile Ser Trp Asn Asp Phe Val His Glu Met Leu Ala
 165 170 175
 Lys Gly Glu Val Gln Arg Val Gln Val Val Pro Glu Ser Asp Val Val
 180 185 190
 Glu Val Tyr Leu His Pro Gly Ala Val Val Phe Gly Arg Pro Arg Leu
 195 200 205
 Ala Leu Met Tyr Arg Met Gln Val Ala Asn Ile Asp Lys Phe Glu Glu
 210 215 220
 Lys Leu Arg Ala Ala Glu Asp Glu Leu Asn Ile Glu Ala Lys Asp Arg
 225 230 235 240
 Ile Pro Val Ser Tyr Lys Arg Thr Gly Phe Phe Gly Asn Ala Leu Tyr
 245 250 255
 Ser Val Gly Met Thr Ala Val Gly Leu Ala Ile Leu Trp Tyr Val Phe
 260 265 270
 Arg Leu Ala Gly Met Thr Gly Arg Glu Gly Gly Phe Ser Ala Phe Asn
 275 280 285
 Gln Leu Lys Met Ala Arg Phe Thr Ile Val Asp Gly Lys Met Gly Lys
 290 295 300
 Gly Val Ser Phe Lys Asp Val Ala Gly Met His Glu Ala Lys Leu Glu
 305 310 315 320
 Val Arg Glu Phe Val Asp Tyr Leu Lys Ser Pro Glu Arg Phe Leu Gln
 325 330 335

Leu Gly Ala Lys Val Pro Lys Gly Ala Leu Leu Leu Gly Pro Pro Gly
 340 345 350

Cys Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Thr Glu Ala Gln Val
 355 360 365

Pro Phe Leu Ala Met Ala Gly Pro Glu Phe Val Glu Val Ile Gly Gly
 370 375 380

Leu Gly Ala Ala Arg Val Arg Ser Leu Phe Lys Glu Ala Arg Ala Arg
 385 390 395 400

Ala Pro Cys Ile Val Tyr Ile Asp Glu Ile Asp Ala Val Gly Lys Lys
 405 410 415

Arg Ser Thr Thr Met Ser Gly Phe Ser Asn Thr Glu Glu Glu Gln Thr
 420 425 430

Leu Asn Gln Leu Leu Val Glu Met Asp Gly Met Gly Thr Thr Asp His
 435 440 445

Val Ile Val Leu Ala Ser Thr Asn Arg Ala Asp Ile Leu Asp Gly Ala
 450 455 460

Leu Met Arg Pro Gly Arg Leu Asp Arg His Val Phe Ile Asp Leu Pro
 465 470 475 480

Thr Leu Gln Glu Arg Arg Glu Ile Phe Glu Gln His Leu Lys Ser Leu
 485 490 495

Lys Leu Thr Gln Ser Ser Thr Phe Tyr Ser Gln Arg Leu Ala Glu Leu
 500 505 510

Thr Pro Gly Phe Ser Gly Ala Asp Ile Ala Asn Ile Cys Asn Glu Ala
 515 520 525

Ala Leu His Ala Ala Arg Glu Gly His Thr Ser Val His Thr Leu Asn
 530 535 540

Phe Glu Tyr Ala Val Glu Arg Val Leu Ala Gly Thr Ala Lys Lys Ser
 545 550 555 560

Lys Ile Leu Ser Lys Glu Glu Gln Lys Val Val Ala Phe His Glu Ser
 565 570 575

Gly His Ala Leu Val Gly Trp Met Leu Glu His Thr Glu Ala Val Met
 580 585 590

Lys Val Ser Ile Thr Pro Arg Thr Asn Ala Ala Leu Gly Phe Ala Gln
 595 600 605

Met Leu Pro Arg Asp Gln His Leu Phe Thr Lys Glu Gln Leu Phe Glu
 610 615 620

Arg Met Cys Met Ala Leu Gly Gly Arg Ala Ser Glu Ala Leu Ser Phe
 625 630 635 640

Asn Glu Val Thr Ser Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Arg
 645 650 655

Ile Ala Tyr Ser Met Val Lys Gln Phe Gly Met Ala Pro Gly Ile Gly
660 665 670

Pro Ile Ser Phe Pro Glu Ala Gln Glu Gly Leu Met Gly Ile Gly Arg
675 680 685

Arg Pro Phe Ser Gln Gly Leu Gln Gln Met Met Asp His Glu Ala Arg
690 695 700

Leu Leu Val Ala Lys Ala Tyr Arg His Thr Glu Lys Val Leu Gln Asp
705 710 715 720

Asn Leu Asp Lys Leu Gln Ala Leu Ala Asn Ala Leu Leu Glu Lys Glu
725 730 735

Val Ile Asn Tyr Glu Asp Ile Glu Ala Leu Ile Gly Pro Pro Pro His
740 745 750

Gly Pro Lys Lys Met Ile Ala Pro Gln Arg Trp Ile Asp Ala Gln Arg
755 760 765

Glu Lys Gln Asp Leu Gly Glu Glu Glu Thr Glu Glu Thr Gln Gln Pro
770 775 780

Pro Leu Gly Gly Glu Glu Pro Thr Trp Pro Lys
785 790 795

<210> 25
<211> 373
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic CD13
aminopeptidase GH1-72-PCR-G3F1

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tccttgaggg gaggacactg gtgcctcggg ctccaggaat ggaggccctg caccagccgc 180
tgggatggac acatgtgggc acctgcatg ggggccgggt gacttcaagg gctggggact 240
atgtgctgtt ttctgtgaac cactggagca ccacctcctt gttctccttc acccacttat 300
gttgctttcg tcttctccag gggcttgctc cagggcccggt gtgccttagc cgaagcctgt 360
ttcctcgttt cct 373

<210> 26
<211> 967
<212> PRT
<213> Homo sapiens

<220>
<223> aminopeptidase N, microsomal aminopeptidase,
myeloid plasma membrane glycoprotein CD13 (GP150)

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Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
 20 25 30
 Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
 35 40 45
 Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
 50 55 60
 Leu Asp Gln Ser Lys Ala Trp Asn Arg Tyr Arg Leu Pro Asn Thr Leu
 65 70 75 80
 Lys Pro Asp Ser Tyr Gln Val Thr Leu Arg Pro Tyr Leu Thr Pro Asn
 85 90 95
 Asp Arg Gly Leu Tyr Val Phe Lys Gly Ser Ser Thr Val Arg Phe Thr
 100 105 110
 Cys Lys Glu Ala Thr Asp Val Ile Ile Ile His Ser Lys Lys Leu Asn
 115 120 125
 Tyr Thr Leu Ser Gln Gly His Arg Val Val Leu Arg Gly Val Gly Gly
 130 135 140
 Ser Gln Pro Pro Asp Ile Asp Lys Thr Glu Leu Val Glu Pro Thr Glu
 145 150 155 160
 Tyr Leu Val Val His Leu Lys Gly Ser Leu Val Lys Asp Ser Gln Tyr
 165 170 175
 Glu Met Asp Ser Glu Phe Glu Gly Glu Leu Ala Asp Asp Leu Ala Gly
 180 185 190
 Phe Tyr Arg Ser Glu Tyr Met Glu Gly Asn Val Arg Lys Val Val Ala
 195 200 205
 Thr Thr Gln Met Gln Ala Ala Asp Ala Arg Lys Ser Phe Pro Cys Phe
 210 215 220
 Asp Glu Pro Ala Met Lys Ala Glu Phe Asn Ile Thr Leu Ile His Pro
 225 230 235 240
 Lys Asp Leu Thr Ala Leu Ser Asn Met Leu Pro Lys Gly Pro Ser Thr
 245 250 255
 Pro Leu Pro Glu Asp Pro Asn Trp Asn Val Thr Glu Phe His Thr Thr
 260 265 270
 Pro Lys Met Ser Thr Tyr Leu Leu Ala Phe Ile Val Ser Glu Phe Asp
 275 280 285
 Tyr Val Glu Lys Gln Ala Ser Asn Gly Val Leu Ile Arg Ile Trp Ala
 290 295 300
 Arg Pro Ser Ala Ile Ala Ala Gly His Gly Asp Tyr Ala Leu Asn Val
 305 310 315 320
 Thr Gly Pro Ile Leu Asn Phe Phe Ala Gly His Tyr Asp Thr Pro Tyr
 325 330 335

Pro Leu Pro Lys Ser Asp Gln Ile Gly Leu Pro Asp Phe Asn Ala Gly
 340 345 350
 Ala Met Glu Asn Trp Gly Leu Val Thr Tyr Arg Glu Asn Ser Leu Leu
 355 360 365
 Phe Asp Pro Leu Ser Ser Ser Ser Ser Asn Lys Glu Arg Val Val Thr
 370 375 380
 Val Ile Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr
 385 390 395 400
 Ile Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala Ser Tyr
 405 410 415
 Val Glu Tyr Leu Gly Ala Asp Tyr Ala Glu Pro Thr Trp Asn Leu Lys
 420 425 430
 Asp Leu Met Val Leu Asn Asp Val Tyr Arg Val Met Ala Val Asp Ala
 435 440 445
 Leu Ala Ser Ser His Pro Leu Ser Thr Pro Ala Ser Glu Ile Asn Thr
 450 455 460
 Pro Ala Gln Ile Ser Glu Leu Phe Asp Ala Ile Ser Tyr Ser Lys Gly
 465 470 475 480
 Ala Ser Val Leu Arg Met Leu Ser Ser Phe Leu Ser Glu Asp Val Phe
 485 490 495
 Lys Gln Gly Leu Ala Ser Tyr Leu His Thr Phe Ala Tyr Gln Asn Thr
 500 505 510
 Ile Tyr Leu Asn Leu Trp Asp His Leu Gln Glu Ala Val Asn Asn Arg
 515 520 525
 Ser Ile Gln Leu Pro Thr Thr Glu Arg Asp Ile Met Asn Arg Trp Thr
 530 535 540
 Leu Gln Met Gly Phe Pro Val Ile Thr Val Asp Thr Ser Thr Gly Thr
 545 550 555 560
 Leu Ser Gln Glu His Phe Leu Leu Asp Pro Asp Ser Asn Val Thr Arg
 565 570 575
 Pro Ser Glu Phe Asn Tyr Val Trp Ile Val Pro Ile Thr Ser Ile Arg
 580 585 590
 Asp Gly Arg Gln Gln Gln Asp Tyr Trp Leu Met Asp Val Arg Ala Gln
 595 600 605
 Asn Asp Leu Phe Ser Thr Ser Gly Asn Glu Trp Val Leu Leu Asn Leu
 610 615 620
 Asn Val Thr Gly Tyr Tyr Arg Val Asn Tyr Asp Glu Glu Asn Trp Arg
 625 630 635 640
 Lys Ile Gln Thr Gln Leu Gln Arg Asp His Ser Ala Ile Pro Val Ile
 645 650 655

Asn Arg Ala Gln Ile Ile Asn Asp Ala Phe Asn Leu Ala Ser Ala His
 660 665 670
 Lys Val Pro Val Thr Leu Ala Leu Asn Asn Thr Leu Phe Leu Ile Glu
 675 680 685
 Glu Arg Gln Tyr Met Pro Trp Glu Ala Ala Leu Ser Ser Leu Ser Tyr
 690 695 700
 Phe Lys Leu Met Phe Asp Arg Ser Glu Val Tyr Gly Pro Met Lys Asn
 705 710 715 720
 Tyr Leu Lys Lys Gln Val Thr Pro Leu Phe Ile His Phe Arg Asn Asn
 725 730 735
 Thr Asn Asn Trp Arg Glu Ile Pro Glu Asn Leu Met Asp Gln Tyr Ser
 740 745 750
 Glu Val Asn Ala Ile Ser Thr Ala Cys Ser Asn Gly Val Pro Glu Cys
 755 760 765
 Glu Glu Met Val Ser Gly Leu Phe Lys Gln Trp Met Glu Asn Pro Asn
 770 775 780
 Asn Asn Pro Ile His Pro Asn Leu Arg Ser Thr Val Tyr Cys Asn Ala
 785 790 795 800
 Ile Ala Gln Gly Gly Glu Glu Glu Trp Asp Phe Ala Trp Glu Gln Phe
 805 810 815
 Arg Asn Ala Thr Leu Val Asn Glu Ala Asp Lys Leu Arg Ala Ala Leu
 820 825 830
 Ala Cys Ser Lys Glu Leu Trp Ile Leu Asn Arg Tyr Leu Ser Tyr Thr
 835 840 845
 Leu Asn Pro Asp Leu Ile Arg Lys Gln Asp Ala Thr Ser Thr Ile Ile
 850 855 860
 Ser Ile Thr Asn Asn Val Ile Gly Gln Gly Leu Val Trp Asp Phe Val
 865 870 875 880
 Gln Ser Asn Trp Lys Lys Pro Phe Asn Asp Tyr Gly Gly Gly Ser Phe
 885 890 895
 Ser Phe Ser Asn Leu Ile Gln Ala Val Thr Arg Arg Phe Ser Thr Glu
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 Tyr Glu Leu Gln Gln Leu Glu Gln Phe Lys Lys Asp Asn Glu Glu Thr
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 Gly Phe Gly Ser Gly Thr Arg Ala Leu Glu Gln Ala Leu Glu Lys Thr
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 Trp Phe Thr Glu Asn Ser Lys
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<210> 27
 <211> 3494
 <212> DNA
 <213> Homo sapiens

<220>
 <223> alanyl (membrane) aminopeptidase, aminopeptidase
 M, microsomal aminopeptidase, CD13, p150 (ANPEP)
 cDNA

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<210> 28

<211> 967

<212> PRT

<213> Homo sapiens

<220>

<223> membrane alanine aminopeptidase precursor,
 aminopeptidase N, aminopeptidase M, microsomal
 aminopeptidase, alanyl (membrane) aminopeptidase

<400> 28

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Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
             20             25             30

Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
             35             40             45

Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
             50             55             60

Leu Asp Gln Ser Lys Ala Trp Asn Arg Tyr Arg Leu Pro Asn Thr Leu
             65             70             75             80

Lys Pro Asp Ser Tyr Gln Val Thr Leu Arg Pro Tyr Leu Thr Pro Asn
             85             90             95

Asp Arg Gly Leu Tyr Val Phe Lys Gly Ser Ser Thr Val Arg Phe Thr
             100            105            110

Cys Lys Glu Ala Thr Asp Val Ile Ile Ile His Ser Lys Lys Leu Asn
             115            120            125

Tyr Thr Leu Ser Gln Gly His Arg Val Val Leu Arg Gly Val Gly Gly
             130            135            140

Ser Gln Pro Pro Asp Ile Asp Lys Thr Glu Leu Val Glu Pro Thr Glu
             145            150            155            160

Tyr Leu Val Val His Leu Lys Gly Ser Leu Val Lys Asp Ser Gln Tyr
             165            170            175

Glu Met Asp Ser Glu Phe Glu Gly Glu Leu Ala Asp Asp Leu Ala Gly
             180            185            190

Phe Tyr Arg Ser Glu Tyr Met Glu Gly Asn Val Arg Lys Val Val Ala
             195            200            205

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Ser	Ile	Gln	Leu	Pro	Thr	Thr	Val	Arg	Asp	Ile	Met	Asn	Arg	Trp	Thr	530	535	540
Leu	Gln	Met	Gly	Phe	Pro	Val	Ile	Thr	Val	Asp	Thr	Ser	Thr	Gly	Thr	545	550	555
Leu	Ser	Gln	Glu	His	Phe	Leu	Leu	Asp	Pro	Asp	Ser	Asn	Val	Thr	Arg	565	570	575
Pro	Ser	Glu	Phe	Asn	Tyr	Val	Trp	Ile	Val	Pro	Ile	Thr	Ser	Ile	Arg	580	585	590
Asp	Gly	Arg	Gln	Gln	Gln	Asp	Tyr	Trp	Leu	Ile	Asp	Val	Arg	Ala	Gln	595	600	605
Asn	Asp	Leu	Phe	Ser	Thr	Ser	Gly	Asn	Glu	Trp	Val	Leu	Leu	Asn	Leu	610	615	620
Asn	Val	Thr	Gly	Tyr	Tyr	Arg	Val	Asn	Tyr	Asp	Glu	Glu	Asn	Trp	Arg	625	630	635
Lys	Ile	Gln	Thr	Gln	Leu	Gln	Arg	Asp	His	Ser	Ala	Ile	Pro	Val	Ile	645	650	655
Asn	Arg	Ala	Gln	Ile	Ile	Asn	Asp	Ala	Phe	Asn	Leu	Ala	Ser	Ala	His	660	665	670
Lys	Val	Pro	Val	Thr	Leu	Ala	Leu	Asn	Asn	Thr	Leu	Phe	Leu	Ile	Glu	675	680	685
Glu	Arg	Gln	Tyr	Met	Pro	Trp	Glu	Ala	Ala	Leu	Ser	Ser	Leu	Ser	Tyr	690	695	700
Phe	Lys	Leu	Met	Phe	Asp	Arg	Ser	Glu	Val	Tyr	Gly	Pro	Met	Lys	Asn	705	710	715
Tyr	Leu	Lys	Lys	Gln	Val	Thr	Pro	Leu	Phe	Ile	His	Phe	Arg	Asn	Asn	725	730	735
Thr	Asn	Asn	Trp	Arg	Glu	Ile	Pro	Glu	Asn	Leu	Met	Asp	Gln	Tyr	Ser	740	745	750
Glu	Val	Asn	Ala	Ile	Ser	Thr	Ala	Cys	Ser	Asn	Gly	Val	Pro	Glu	Cys	755	760	765
Glu	Glu	Met	Val	Ser	Gly	Leu	Phe	Lys	Gln	Trp	Met	Glu	Asn	Pro	Asn	770	775	780
Asn	Asn	Pro	Ile	His	Pro	Asn	Leu	Arg	Ser	Thr	Val	Tyr	Cys	Asn	Ala	785	790	795
Ile	Ala	Gln	Gly	Gly	Glu	Glu	Glu	Trp	Asp	Phe	Ala	Trp	Glu	Gln	Phe	805	810	815
Arg	Asn	Ala	Thr	Leu	Val	Asn	Glu	Ala	Asp	Lys	Leu	Arg	Ala	Ala	Leu	820	825	830
Ala	Cys	Ser	Lys	Glu	Leu	Trp	Ile	Leu	Asn	Arg	Tyr	Leu	Ser	Tyr	Thr	835	840	845

Leu Asn Pro Asp Leu Ile Arg Lys Gln Asp Ala Thr Ser Thr Ile Ile
 850 855 860
 Ser Ile Thr Asn Asn Val Ile Gly Gln Gly Leu Val Trp Asp Phe Val
 865 870 875 880
 Gln Ser Asn Trp Lys Lys Leu Phe Asn Asp Tyr Gly Gly Gly Ser Phe
 885 890 895
 Ser Phe Ser Asn Leu Ile Gln Ala Val Thr Arg Arg Phe Ser Thr Glu
 900 905 910
 Tyr Glu Leu Gln Gln Leu Glu Gln Phe Lys Lys Asp Asn Glu Glu Thr
 915 920 925
 Gly Phe Gly Ser Gly Thr Arg Ala Leu Glu Gln Ala Leu Glu Lys Thr
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 Lys Ala Asn Ile Lys Trp Val Lys Glu Asn Lys Glu Val Val Leu Gln
 945 950 955 960
 Trp Phe Thr Glu Asn Ser Lys
 965

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 <211> 263
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic PRK-1
 GH1-54-PCR-G3F1

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 tcaatggggg gacctgggac cccagacagc gcccccttc ctgagccgcc cagcccgggg 180
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 tgatactcac tgacgtgata cgt 263

<210> 30
 <211> 3001
 <212> DNA
 <213> Homo sapiens

<220>
 <223> protein kinase C-like 1 (PRKCL1), PRK-1 cDNA

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3001

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<210> 31
<211> 942
<212> PRT
<213> Homo sapiens

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<220>
<223> protein kinase C-like 1 (PRKCL1), serine-threonine
      kinase N, PRK-1

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Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys
  35               40              45

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 65 70 75 80
 Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala
 85 90 95
 His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser
 100 105 110
 Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val
 115 120 125
 Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly
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 Ala Glu Asn Met Ile Gln Thr Tyr Ser Asn Gly Ser Thr Lys Asp Arg
 145 150 155 160
 Lys Leu Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys
 165 170 175
 Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Asp Gln
 180 185 190
 Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu
 195 200 205
 Gly Ala Val Glu Leu Arg Ile Glu Glu Leu Arg His His Phe Arg Val
 210 215 220
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 225 230 235 240
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 245 250 255
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 Ala Gly Pro Phe Pro Ala Thr His Tyr Ser Thr Leu Cys Lys Pro Ala
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 Pro Leu Thr Gly Thr Leu Glu Val Arg Val Val Gly Cys Arg Asp Leu
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 Thr Pro Asp Ser Arg Pro Pro Phe Leu Ser Arg Pro Ala Arg Gly Leu
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Tyr Ser Arg Ser Gly Ser Leu Ser Gly Arg Ser Ser Leu Lys Ala Glu
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 Val Val Gly Gln Thr Ser Trp Lys Pro Cys Gly Pro Asn Ala Trp Asp
 405 410 415
 Gln Ser Phe Thr Leu Glu Leu Glu Arg Ala Arg Glu Leu Glu Leu Ala
 420 425 430
 Val Phe Trp Arg Asp Gln Arg Gly Leu Cys Ala Leu Lys Phe Leu Lys
 435 440 445
 Leu Glu Asp Phe Leu Asp Asn Glu Arg His Glu Val Gln Leu Asp Met
 450 455 460
 Glu Pro Gln Gly Cys Leu Val Ala Glu Val Thr Phe Arg Asn Pro Val
 465 470 475 480
 Ile Glu Arg Ile Pro Arg Leu Arg Arg Gln Lys Lys Ile Phe Ser Lys
 485 490 495
 Gln Gln Gly Lys Ala Phe Gln Arg Ala Arg Gln Met Asn Ile Asp Val
 500 505 510
 Ala Thr Trp Val Arg Leu Leu Arg Arg Leu Ile Pro Asn Ala Thr Gly
 515 520 525
 Thr Gly Thr Phe Ser Pro Gly Ala Ser Pro Gly Ser Glu Ala Arg Thr
 530 535 540
 Thr Gly Asp Ile Ser Val Glu Lys Leu Asn Leu Gly Thr Asp Ser Asp
 545 550 555 560
 Ser Ser Pro Gln Lys Ser Ser Arg Asp Pro Pro Ser Ser Pro Ser Ser
 565 570 575
 Leu Ser Ser Pro Ile Gln Glu Ser Thr Ala Pro Glu Leu Pro Ser Glu
 580 585 590
 Thr Gln Glu Thr Pro Gly Pro Ala Leu Cys Ser Pro Leu Arg Lys Ser
 595 600 605
 Pro Leu Thr Leu Glu Asp Phe Lys Phe Leu Ala Val Leu Gly Arg Gly
 610 615 620
 His Phe Gly Lys Val Leu Leu Ser Glu Phe Arg Pro Ser Gly Glu Leu
 625 630 635 640
 Phe Ala Ile Lys Ala Leu Lys Lys Gly Asp Ile Val Ala Arg Asp Glu
 645 650 655
 Val Glu Ser Leu Met Cys Glu Lys Arg Ile Leu Ala Ala Val Thr Ser
 660 665 670
 Ala Gly His Pro Phe Leu Val Asn Leu Phe Gly Cys Phe Gln Thr Pro
 675 680 685

Glu His Val Cys Phe Val Met Glu Tyr Ser Ala Gly Gly Asp Leu Met
690 695 700

Leu His Ile His Ser Asp Val Phe Ser Glu Pro Arg Ala Ile Phe Tyr
705 710 715 720

Ser Ala Cys Val Val Leu Gly Leu Gln Phe Leu His Glu His Lys Ile
725 730 735

Val Tyr Arg Asp Leu Lys Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly
740 745 750

Tyr Val Lys Ile Ala Asp Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr
755 760 765

Gly Asp Arg Thr Ser Thr Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro
770 775 780

Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly
785 790 795 800

Leu Gly Val Leu Leu Tyr Glu Met Leu Val Gly Glu Ser Pro Phe Pro
805 810 815

Gly Asp Asp Glu Glu Glu Val Phe Asp Ser Ile Val Asn Asp Glu Val
820 825 830

Arg Tyr Pro Arg Phe Leu Ser Ala Glu Ala Ile Gly Ile Met Arg Arg
835 840 845

Leu Leu Arg Arg Asn Pro Glu Arg Arg Leu Gly Ser Ser Glu Arg Asp
850 855 860

Ala Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu
865 870 875 880

Ala Leu Leu Ala Arg Arg Leu Pro Pro Phe Val Pro Thr Leu Ser
885 890 895

Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala
900 905 910

Pro Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu
915 920 925

Gln Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
930 935 940

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<211> 454

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic Zip
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<210> 33

<211> 2105

<212> DNA

<213> Homo sapiens

<220>

<223> death-associated protein kinase 3 (DAPK3) cDNA

<400> 33

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gcggggaacg agttcaagaa catcttcggc accccggagt ttgtggcccc agagattgtg 660
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<210> 34

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> death-associated protein kinase 3 (DAPK3)

<400> 34

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Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln
      20             25             30

Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg
      35             40             45

Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
      50             55             60

Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
      65             70             75             80

Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
      85             90             95

Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
      100            105            110

Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
      115            120            125

Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
      130            135            140

Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
      145            150            155            160

Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
      165            170            175

Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
      180            185            190

Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
      195            200            205

Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
      210            215            220

Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
      225            230            235            240

Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
      245            250            255

Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
      260            265            270

Ser Trp Ile Lys Ala Ile Arg Arg Arg Asn Val Arg Gly Glu Asp Ser
      275            280            285

Gly Arg Lys Pro Glu Arg Arg Arg Leu Lys Thr Thr Arg Leu Lys Glu
      290            295            300

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Tyr Thr Ile Lys Ser His Ser Ser Leu Pro Pro Asn Asn Ser Tyr Ala
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 Asp Phe Glu Arg Phe Ser Lys Val Leu Glu Glu Ala Ala Ala Ala Glu
 325 330 335
 Glu Gly Leu Arg Glu Leu Gln Arg Ser Arg Arg Leu Cys His Glu Asp
 340 345 350
 Val Glu Ala Leu Ala Ala Ile Tyr Glu Glu Lys Glu Ala Trp Tyr Arg
 355 360 365
 Glu Glu Ser Asp Ser Leu Gly Gln Asp Leu Arg Arg Leu Arg Gln Glu
 370 375 380
 Leu Leu Lys Thr Glu Ala Leu Lys Arg Gln Ala Gln Glu Glu Ala Lys
 385 390 395 400
 Gly Ala Leu Leu Gly Thr Ser Gly Leu Lys Arg Arg Phe Ser Arg Leu
 405 410 415
 Glu Asn Arg Tyr Glu Ala Leu Ala Lys Gln Val Ala Ser Glu Met Arg
 420 425 430
 Phe Val Gln Asp Leu Val Arg Ala Leu Glu Gln Glu Lys Leu Gln Gly
 435 440 445
 Val Glu Cys Gly Leu Arg
 450

<210> 35
 <211> 2105
 <212> DNA
 <213> Homo sapiens

<220>
 <223> ZIP-kinase cDNA

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 gaggaccatt atgagatggg ggaggagctg ggcagcggcc agtttgcat cgtgcggaag 180
 tgccggcaga agggcacggg caaggagtac gcagccaagt tcatcaagaa gcgccgcctg 240
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<210> 36

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> ZIP-kinase

<400> 36

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Met Ser Thr Phe Arg Gln Glu Asp Val Glu Asp His Tyr Glu Met Gly
  1             5             10             15

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Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln
      20             25             30

```

```

Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg
      35             40             45

```

```

Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
      50             55             60

```

```

Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
      65             70             75             80

```

```

Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
      85             90             95

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Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
     100             105             110

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Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
     115             120             125

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Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
     130             135             140

```

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Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
     145             150             155             160

```

```

Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
     165             170             175

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Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
     180             185             190

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Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 195 200 205
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
 210 215 220
 Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
 225 230 235 240
 Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
 245 250 255
 Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
 260 265 270
 Ser Trp Ile Lys Ala Ile Arg Arg Arg Asn Val Arg Gly Glu Asp Ser
 275 280 285
 Gly Arg Lys Pro Glu Arg Arg Arg Leu Lys Thr Thr Arg Leu Lys Glu
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 Tyr Thr Ile Lys Ser His Ser Ser Leu Pro Pro Asn Asn Ser Tyr Ala
 305 310 315 320
 Asp Phe Glu Arg Phe Ser Lys Val Leu Glu Glu Ala Ala Ala Ala Glu
 325 330 335
 Glu Gly Leu Arg Glu Leu Gln Arg Ser Arg Arg Leu Cys His Glu Asp
 340 345 350
 Val Glu Ala Leu Ala Ala Ile Tyr Glu Glu Lys Glu Ala Trp Tyr Arg
 355 360 365
 Glu Glu Ser Asp Ser Leu Gly Gln Asp Leu Arg Arg Leu Arg Gln Glu
 370 375 380
 Leu Leu Lys Thr Glu Ala Leu Lys Arg Gln Ala Gln Glu Glu Ala Lys
 385 390 395 400
 Gly Ala Leu Leu Gly Thr Ser Gly Leu Lys Arg Arg Phe Ser Arg Leu
 405 410 415
 Glu Asn Arg Tyr Glu Ala Leu Ala Lys Gln Val Ala Ser Glu Met Arg
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 Phe Val Gln Asp Leu Val Arg Ala Leu Glu Gln Glu Lys Leu Gln Gly
 435 440 445
 Val Glu Cys Gly Leu Arg
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<210> 37

<211> 2055

<212> DNA

<213> Homo sapiens

<220>

<223> ZIP kinase cDNA

<400> 37

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<210> 38

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<223> ZIP kinase

<400> 38

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Met Ser Thr Phe Arg Gln Glu Asp Val Glu Asp His Tyr Glu Met Gly
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Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg Lys Cys Arg Gln
      20             25             30

Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg
      35             40             45

Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
      50             55             60

Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile Ile Thr Leu His
      65             70             75             80

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Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile Leu Glu Leu Val
 85 90 95
 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr
 100 105 110
 Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu Asp Gly Val His
 115 120 125
 Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 130 135 140
 Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg Ile Lys Leu Ile
 145 150 155 160
 Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn Glu Phe Lys Asn
 165 170 175
 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 180 185 190
 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 195 200 205
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu Thr Lys Gln Glu
 210 215 220
 Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe Asp Glu Glu Tyr
 225 230 235 240
 Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
 245 250 255
 Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln Ser Leu Glu His
 260 265 270
 Ser Trp Ile Lys Ala Ile Arg Arg Arg Asn Val Arg Gly Glu Asp Ser
 275 280 285
 Gly Arg Lys Pro Glu Arg Arg Arg Leu Lys Thr Thr Arg Leu Lys Glu
 290 295 300
 Tyr Thr Ile Lys Ser His Ser Ser Leu Pro Pro Asn Asn Ser Tyr Ala
 305 310 315 320
 Asp Phe Glu Arg Phe Ser Lys Val Leu Glu Glu Ala Ala Ala Glu
 325 330 335
 Glu Gly Leu Arg Glu Leu Gln Arg Ser Arg Arg Leu Cys His Glu Asp
 340 345 350
 Val Glu Ala Leu Ala Ala Ile Tyr Glu Glu Lys Glu Ala Trp Tyr Arg
 355 360 365
 Glu Glu Ser Asp Ser Leu Gly Gln Asp Leu Arg Arg Leu Arg Gln Glu
 370 375 380
 Leu Leu Lys Thr Glu Ala Leu Lys Arg Gln Ala Gln Glu Glu Ala Lys
 385 390 395 400

Gly Ala Leu Leu Gly Thr Ser Gly Leu Lys Arg Arg Phe Ser Arg Leu
 405 410 415

Glu Asn Arg Tyr Glu Ala Leu Ala Lys Gln Val Ala Ser Glu Met Arg
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Phe Val Gln Asp Leu Val Arg Ala Leu Glu Gln Glu Lys Leu Gln Gly
 435 440 445

Val Glu Cys Gly Leu Arg
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<210> 39
 <211> 196
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic Gas6
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<210> 40
 <211> 2461
 <212> DNA
 <213> Homo sapiens

<220>
 <223> growth arrest-specific 6 (GAS6) cDNA

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Cys Val Glu Glu Leu Cys Ser Arg Glu Glu Ala Arg Glu Val Phe Glu
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Val Glu Pro Ala Ala Ala
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<211> 1960

<212> PRT

<213> Homo sapiens

<220>

<223> myosin, heavy polypeptide 9, non-muscle (MYH9)

<400> 49

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 595 600 605
 Ser Glu Leu Trp Lys Asp Val Asp Arg Ile Ile Gly Leu Asp Gln Val
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 675 680 685
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 Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr
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 Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp
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 Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
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<400> 54

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<210> 55

<211> 482

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic novel Zn
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<400> 55

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<211> 253

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic novel
sugar transporter GH1-175-PCR-G3F1

<400> 56

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<210> 57

<211> 7554

<212> DNA

<213> Homo sapiens

<220>

<223> plexin-A2

<400> 57

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<210> 58

<211> 1895

<212> PRT

<213> Homo sapiens

<220>

<223> plexin-A2

<400> 58

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```

```

Ser Val Val Leu Leu Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala
              20              25              30

```

```

Ala Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp
  35              40              45

```

```

Thr Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val
  50              55              60

```

```

Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln
  65              70              75              80

```

```

Val Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro
              85              90              95

```

```

Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn
 100              105              110

```

```

Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala
 115              120              125

```

```

Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp
 130              135              140

```

```

Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser
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```

```

Ser Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu
 165              170              175

```

```

Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln
 180              185              190

```

```

Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu
 195              200              205

```

```

Ser Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser
 210              215              220

```

```

Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala Leu Val Ser His Phe Asp
 225              230              235              240

```

Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu
 245 250 255
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 260 265 270
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 275 280 285
 Lys Phe His Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly
 290 295 300
 Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp
 305 310 315 320
 Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser Gln Asp Asp Val Leu Phe
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 Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp Asp
 340 345 350
 Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln Ile Lys
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 Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu Glu Leu Asn
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 385 390 395 400
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 405 410 415
 Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr Thr Ser Arg Asp Arg Met
 420 425 430
 Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly Tyr Ser Val Val Phe Val
 435 440 445
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 450 455 460
 His Gly Gly Val Gln Tyr Glu Met Val Ser Val Leu Lys Asp Gly Ser
 465 470 475 480
 Pro Ile Leu Arg Asp Met Ala Phe Ser Ile Asp Gln Arg Tyr Leu Tyr
 485 490 495
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 Gln Tyr Thr Thr Cys Gly Glu Cys Leu Ser Ser Gly Asp Pro His Cys
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 Gly Trp Cys Ala Leu His Asn Met Cys Ser Arg Arg Asp Lys Cys Gln
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 His Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr Thr Cys
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 Ser Phe Gln Glu Gly Arg Ile Asn Ile Ser Glu Asp Cys Pro Gln Leu
 690 695 700
 Val Pro Thr Glu Glu Ile Leu Ile Pro Val Gly Glu Val Lys Pro Ile
 705 710 715 720
 Thr Leu Lys Ala Arg Asn Leu Pro Gln Pro Gln Ser Gly Gln Arg Gly
 725 730 735
 Tyr Glu Cys Val Leu Asn Ile Gln Gly Ala Ile His Arg Val Pro Ala
 740 745 750
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 755 760 765
 Tyr Asp Gly Met Asp Ile Ser Asn Leu Ala Val Asp Phe Ala Val Val
 770 775 780
 Trp Asn Gly Asn Phe Ile Ile Asp Asn Pro Gln Asp Leu Lys Val His
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 805 810 815
 Ala Asp Arg Lys Phe Glu Cys Gly Trp Cys Ser Gly Glu Arg Arg Cys
 820 825 830
 Thr Leu His Gln His Cys Thr Ser Pro Ser Ser Pro Trp Leu Asp Trp
 835 840 845
 Ser Ser His Asn Val Lys Cys Ser Asn Pro Gln Ile Thr Glu Ile Leu
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Pro	Val	Arg	Leu	Cys	Ile	Gly	Glu	Cys	Lys	Pro	Glu	Phe	Met	Thr	Lys	930	935	940	
Ser	His	Gln	Gln	Tyr	Thr	Phe	Val	Asn	Pro	Ser	Val	Leu	Ser	Leu	Asn	945	950	955	960
Pro	Ile	Arg	Gly	Pro	Glu	Ser	Gly	Gly	Thr	Met	Val	Thr	Ile	Thr	Gly	965	970	975	
His	Tyr	Leu	Gly	Ala	Gly	Ser	Ser	Val	Ala	Val	Tyr	Leu	Gly	Asn	Gln	980	985	990	
Thr	Cys	Glu	Phe	Tyr	Gly	Arg	Ser	Met	Ser	Glu	Ile	Val	Cys	Val	Ser	995	1000	1005	
Pro	Pro	Ser	Ser	Asn	Gly	Leu	Gly	Pro	Val	Pro	Val	Ser	Val	Ser	Val	1010	1015	1020	
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Pro	Arg	Val	Gln	Arg	Ile	Glu	Pro	Glu	Trp	Ser	Ile	Ala	Ser	Gly	His	1045	1050	1055	
Thr	Pro	Leu	Thr	Ile	Thr	Gly	Phe	Asn	Leu	Asp	Val	Ile	Gln	Glu	Pro	1060	1065	1070	
Arg	Ile	Arg	Val	Lys	Phe	Asn	Gly	Lys	Glu	Ser	Val	Asn	Val	Cys	Lys	1075	1080	1085	
Val	Val	Asn	Thr	Thr	Thr	Leu	Thr	Cys	Leu	Ala	Pro	Ser	Leu	Thr	Thr	1090	1095	1100	
Asp	Tyr	Arg	Pro	Gly	Leu	Asp	Thr	Val	Glu	Arg	Pro	Asp	Glu	Phe	Gly	1105	1110	1115	1120
Phe	Val	Phe	Asn	Asn	Val	Gln	Ser	Leu	Leu	Ile	Tyr	Asn	Asp	Thr	Lys	1125	1130	1135	
Phe	Ile	Tyr	Tyr	Pro	Asn	Pro	Thr	Phe	Glu	Leu	Leu	Ser	Pro	Thr	Gly	1140	1145	1150	
Val	Leu	Asp	Gln	Lys	Pro	Gly	Ser	Pro	Ile	Ile	Leu	Lys	Gly	Lys	Asn	1155	1160	1165	
Leu	Cys	Pro	Pro	Ala	Ser	Gly	Gly	Ala	Lys	Leu	Asn	Tyr	Thr	Val	Leu	1170	1175	1180	
Ile	Gly	Glu	Thr	Pro	Cys	Ala	Val	Thr	Val	Ser	Glu	Thr	Gln	Leu	Leu	1185	1190	1195	1200

Cys Glu Pro Pro Asn Leu Thr Gly Gln His Lys Val Met Val His Val
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 Gly Gly Met Val Phe Ser Pro Gly Ser Val Ser Val Ile Ser Asp Ser
 1220 1225 1230
 Leu Leu Thr Leu Pro Ala Ile Val Ser Ile Ala Ala Gly Gly Ser Leu
 1235 1240 1245
 Leu Leu Ile Ile Val Ile Ile Val Leu Ile Ala Tyr Lys Arg Lys Ser
 1250 1255 1260
 Arg Glu Asn Asp Leu Thr Leu Lys Arg Leu Gln Met Gln Met Asp Asn
 1265 1270 1275 1280
 Leu Glu Ser Arg Val Ala Leu Glu Cys Lys Glu Ala Phe Ala Glu Leu
 1285 1290 1295
 Gln Thr Asp Ile Asn Glu Leu Thr Ser Asp Leu Asp Arg Ser Gly Ile
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 Pro Tyr Leu Asp Tyr Arg Thr Tyr Ala Met Arg Val Leu Phe Pro Gly
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 Gln Gln His Val Glu Lys Ala Leu Lys Leu Phe Ala Gln Leu Ile Asn
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 Ser Phe Ser Met Arg Asp Arg Gly Asn Val Ala Ser Leu Ile Met Thr
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 1475 1480 1485
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 Tyr Lys Asn Val Pro Tyr Ser Gln Arg Pro Arg Ala Val Asp Met Asp
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 Gln Thr Phe Met Asp Ser Cys Ser Thr Ser Glu His Arg Leu Gly Lys
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 Lys Ser Trp Val Glu Arg Tyr Tyr Ala Asp Ile Ala Lys Leu Pro Ala
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 Ile Ser Asp Gln Asp Met Asn Ala Tyr Leu Ala Glu Gln Ser Arg Leu
 1825 1830 1835 1840

His Ala Val Glu Phe Asn Met Leu Ser Ala Leu Asn Glu Ile Tyr Ser
 1845 1850 1855

Tyr Val Ser Lys Tyr Ser Glu Glu Leu Ile Gly Ala Leu Glu Gln Asp
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Glu Gln Ala Arg Arg Gln Arg Leu Ala Tyr Lys Val Glu Gln Leu Ile
 1875 1880 1885

Asn Ala Met Ser Ile Glu Ser
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Pro Asn Ser Gln Val Gly Ala Cys Ile Val Asn Ser Glu Asn Lys Ile
 35 40 45

Val Gly Ile Gly Tyr Asn Gly Met Pro Asn Gly Cys Ser Asp Asp Val
 50 55 60

Leu Pro Trp Arg Arg Thr Ala Glu Asn Lys Leu Asp Thr Lys Tyr Pro
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Tyr Val Cys His Ala Glu Leu Asn Ala Ile Met Asn Lys Asn Ser Thr
 85 90 95

Asp Val Lys Gly Cys Ser Met Tyr Val Ala Leu Phe Pro Cys Asn Glu
 100 105 110

Cys Ala Lys Leu Ile Ile Gln Ala Gly Ile Lys Glu Val Ile Phe Thr
 115 120 125

Ser Asp Lys Tyr His Asp Ser Asp Glu Ala Thr Ala Ala Arg Leu Leu
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Phe Asn Met Ala Gly Val Thr Phe Arg Lys Phe Ile Pro Lys Cys Ser
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<400> 71
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